TITLE: DELETIONS IN ARTERIVIRUS REPLICONS

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| expression | + | + | 1 | + | | |
|---------------|--|---------------|--|---------------|---|---|
| expression | + | ı | a- | 1 | ે. - | |
| number | 437 | 594 | 521 | 664 | 899 | |
| (nucleotides) | t | Δ 11788-14139 | - TETAAA A 14585-14984 | Δ 11788-14584 | - AAA \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ | |
| | STUTR- ORFIAD, ORF2 ORF3 ORF4 ORF5 ORF6 ORF7 3'UTR | | What is the second of the seco | | | 1) Identical results were obtained in IPMA using MAbs against GP3 and GP4 |

Fig. 1A

REPLICONS

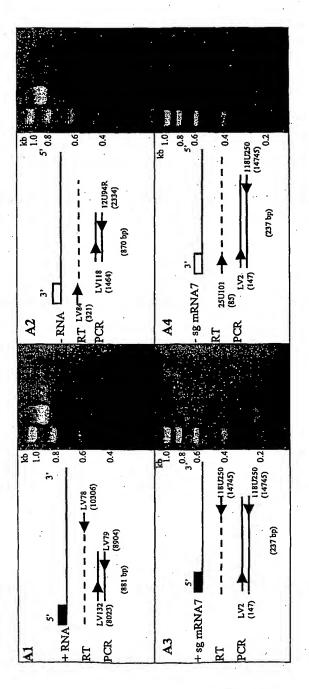
Inventor: Monique Helene Verheije Docket No.: 2183-6217US

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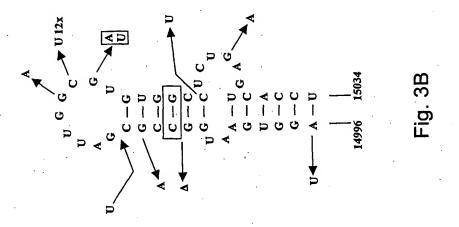
| Constructs | Deletion (nucleotides) | PABV number | M- expression |
|--|---------------------------|----------------|-------------------|
| S'UTR- ORF6 Hpd ATG ORF7 Pact JAA3'UTR ATG ORF7 Pact JAA3'UTR | · - | 437 | +1) |
| Zani ning and | Δ 14588-14936 | 605 | · - |
| // | Δ 14588-14885 | 604 | • |
| AAA | Δ 14588-14786 | 603 | - |
| AAA TORRA TO | Δ 14588-14687 | 602 | • |
| AAA | Δ 14588-14642 | 624 | + |
| AAA | Δ 14599-14642 | 625 | + |
| STORT DESCRIPTION OF STATE OF | Δ 14588-14600 | 626 | +1) |
| TO THE R AAA | Δ 14938-14980 | 638 | + ¹⁾ . |
| TE SHOULD AAA | Δ 14887-14980 | 637 | + |
| //A | Δ 14788-14980 | 636 | + |
| //- 1 AAA | Δ 14686-14980 | 635 | + |
| AAAA | Δ 14643-14686 | 631 | - |
| MAA | Δ 14643-14676 | 632 | • |
| AAA | Δ 14643-14664 | 633 | •• |
| When I are a second with the contract of the c | Δ 14643-14652 | 634 | + |
| // | Δ 14653-14686 | .696 | - |
| // | rescue of 696 | 730 | +1) |

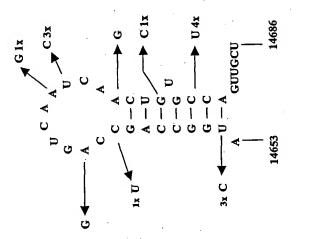
1) Identical results were obtained in IPMA using MAb 122.17 against N

Fig. 2

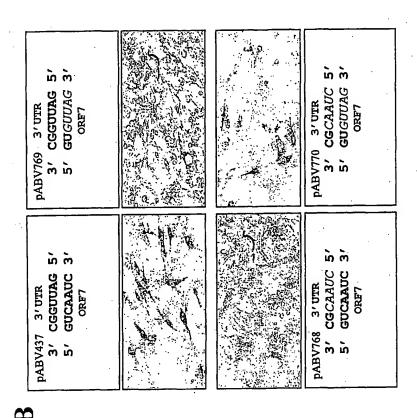


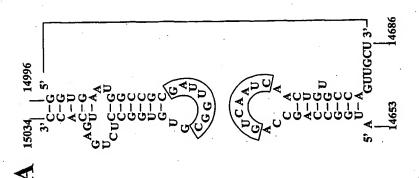
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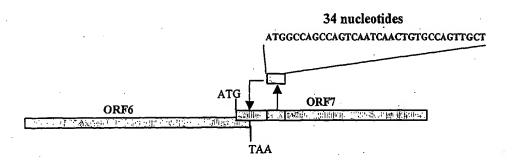


Fig. 5

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| | | Fig. 6 | |
|-------------|-----|--|------------------|
| | | GTGACCGAAATTAAAAAAA: 122 GCGGCCGAAATTAAAAAAA: 159 * * ********************************* | LV VR2332 |
| . 0.0 | 102 | TGTGGCCTCTGAGTCACCTATTCAATTAGGGCGATCACATGGGGGGTCATACTTAATCAGGCAGG | LV VR2332 |
| 32 70 | 32 | TTAAACAGTCA | LV VR2332 |
| , | • | | M |
| | | LTQTERSLCLOSIQTAFNOGAGTASLSSSGKVSFQVEFMLPVAHTVRLIRVTSTSASQGAS : 128 FTPSERQLCLSSIQTAFNQGAGTCTLSDSGRISYTVEFSLPTHHTVRLIRVTASPSA : 123 * ** ** *** ************************* | LV VR2332 |
| ~ to | 99 | MAGKNOSOKKKKSTAPMGNGOPVNOLCOLLGAMIKSOROOPRGGOAKKKRPEKPHEPLAAEDDIKHH : MPNNNGKQOKRKKGDGOPVNOLCOMLGKIIAQONOSRGKGPGKKNKKKNPEKPHEPLATEDDVRHH : * * * * * * * * * * * * * * * * * * * | LV VR2332 |

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| Virus production | | + | + | + | + | + | ı | ı | ì | + | ı | |
|--|-------------|----------------|-------------------|-------------------|------------------|--|---|------------------|------------------|--------------|--------------|----|
| N- expression | | + | + | + | + | + | + | + | + | + | | |
| M- expression | | + | + | + | + | + | + | + | + | + | | |
| Plasmid number | | 437 | 639 | 694 | 745 | 746 | 747 | 748 | 695 | 693 | 729 | |
| Deletion (nucleotides / amino acids) | | wild type | Δ14975-14980 / Δ2 | Δ14969-14980 / Δ4 | Δ14966-14980/ Δ5 | Δ14963-14980/ Δ 6 | Δ14960-14980/ Δ7 | Δ14957-14980/ Δ8 | Δ14954-14980/ Δ9 | Δ14989-14995 | Δ14989-15020 | 2= |
| Constructs | A B C TODAL | ORE7 3'UTR AAA | HI AAA | | AAA | THE STATE OF THE S | - 1 1 1 1 1 1 1 1 1 1 | W AAA | # AAA | | /// | |

Fig. 7

REPLICONS

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Growth curves of PRRSV deletion mutants

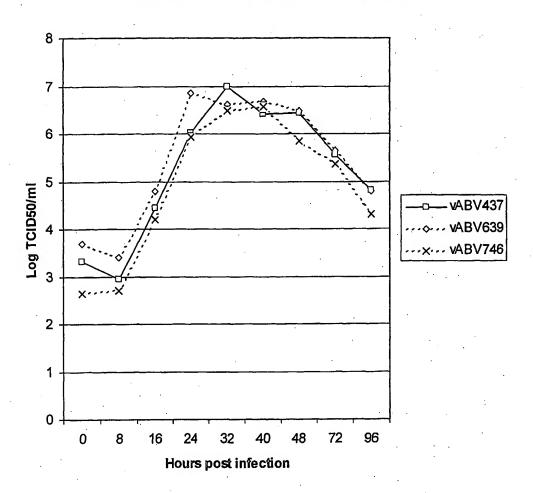
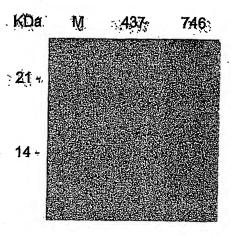


Fig. 8

TITLE: DELETIONS IN ARTERIVIRUS REPLICONS

Inventor: Monique Helene Verheije Docket No.: 2183-6217US

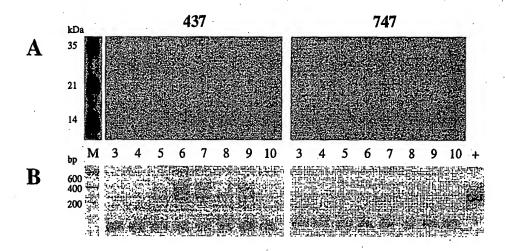
Fig. 9



TITLE: DELETIONS IN ARTERIVIRUS REPLICONS

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Fig. 10



TITLE: DELETIONS IN ARTERIVIRUS REPLICONS

| Primer | Sequence of the primer ^a | Orientation | Purpose (pABV) | Location |
|---------|--|-------------|-------------------|----------|
| 19R218B | s' atracatorageaces? | + | Sequencing | 14782 |
| V20 | S' COTTO TTA A A A GCTTTGA CCCC 3' | | Sequencing | 15066 |
| V75 | SCICILITATION OF STANDED STANDARD OF STANDARD ST | , | Xbal -site | 15088 |
| V155 | s' A CGTGCGTTA A CCTCGTCA A GTA TGGCCGGTA A A A A CCA GA GCCA GA 3' | A3, + | Hpal-site | 14582 |
| VOOA | S'ACGEGNETTA A TELA A CONTROL CEGGGG A TGT A GA S' | 1 | 639 | 14974 |
| 17713 | STACE A GETTA ATTA A GGTGA ATGGCCGCGA 3' | + | 693 | 14996 |
| V 214 | S GACTGTTTA ATTA ACTGGCGGATGTA 3' | | 694 | 14958 |
| V215 | S' GACTGTTTA ATTA AGTCA CGCGA ATC 3' | • | 695 | 14942 |
| V230 | S' TGCA AGTTA ATTA AGCCTCTGAGTCA 3' | + | 729 | 15021 |
| V763 | S' GACTIGITA ATTA AGCIGATIGIA 3' | | 745 | 14954 |
| 77.764 | SUPPLIED ATTARGET OF STATE AGAINST | , | 746 | 14951 |
| 107AC | SIGNOTOTITED ATTARGED AGENCY OF STREET | | 747 | 14948 |
| 1.V266 | 5' GACTGTTTAATTAAGAAGTCACGCGA 3' | • | 748 | 14945 |

^a The restriction sites are underlined.

TITLE: DELETIONS IN ARTERIVIRUS REPLICONS Inventor: Monique Helene Verheije Docket No.: 2183-6217US

Fig. 12

| | Sequence of the primer | Orien- | Purpose | Location |
|---------|--|---------|------------------------------|----------|
| | | tation | (pABV) | |
| | 16 000000000000000000000000000000000000 | | Centencing / Chanden PCR | 14745 |
| 1180250 | 5. CAGCCAGGGAAAAIGIGGC 3 | | Sequencing / Suand-sp. 1 Cr. | 7000 |
| 12U94R | 5' CACCTGTACCTGCTCATTGT 3' | | Strand-sp. PCR | 7334 |
| 251/101 | 5' GTTCTAGCCCAACAGGTATC 3' | + | Strand-sp. RT | 82 |
| 1.00 | 5' AGCGGGAAGGATCCACCGAGTAT 3' | + | Strand-sp. PCR | 147 |
| 1 1 1 1 | s' contribated activities 31 | + | Sequencing | 14045 |
| 11/20 | S COCKE CHOCKE OF THE A A A COUNTY CANCEL ST | + | Sequencing | 15066 |
| 17/75 | S COLONI LIGAÇÃO LO COLO S STATIA GOA ATTICTA GA COLO TOGA | | PCR Xbal -site | 15088 |
| 1111 | 5 TOTAL OLD ATTICE OF THE STATE | , | Ta | 15088 |
| 2,70 | 2 1C1ACCAA11C1ACACCA1CC(1)43 | | Strand-sn RT | 10306 |
| 7 / S | S CCCIGGGAIGAAICIAIGGI | . , | Strand-cn DCD | 8008 |
| 2 2 | S GACAAGAICAICAGAGIAIACC3 | . 4 | Stead or DT | 122 |
| LV84 | S. AGAGCI ICAGGACTORIC | • | DCD D-1 Alto | 14081 |
| CV112 | S' CCATTCACCIGACIGIALAACI IGCACCIGA 3 | | FOR Fact -Site | 14761 |
| LV118 | 5' TTACCACCTACTCTCCACCG 3' | + | Strand-sp. PCK | 404 |
| LV132 | 5' CCTACTGTGCCCTATAGTGTC 3' | + | Strand-sp. PCR. | 8023 |
| LV151 | 5' ACCAGAGCCAGAAGAAAAAGAAAAGTACAGCTGGGTGCAATGAT3' | + | PCR (631) | 14611 |
| LV152 | 5' ACCAGAGCCAGAAAAAAAAAAAAAAAAAAAAAAAAAAA | + | PCR (632) | 14611 |
| LV153 | S' ACCAGAGCCAGAAAAAAAAAAAAAAAGTACAGCTTCAATCAA | + | PCR (633) | . 14611 |
| LV154 | 5' ACCAGAGCCAGAAAAAAAAAAAAAAAGTACAGCTATGGCCAGCCA | + | PCR (634) | 14611 |
| LV155 | 5' ACGTGCGTTAACCTCGTCAAGTATGGCCGGTAAAAAACCAGAGGCCAGA 3 | + | Hpal-site PCR | 14582 |
| LV188 | S' ACGTGCGTTAACTAAGGTGCAATGATAAAGTCCCA 3' | + | PCR (602) | 14582 |
| LV189 | 5' ACGTGCGTTAACTAAATCCCGGCACCACCTCACCCA 3' | + | PCR (603) | 14582 |
| LV190 | S' ACGTGCGTTAACTAAGGGAAGGTCAGTTTTCAGGT 3' | + | PCR (604) | 14582 |
| LV191 | 5' ACGTGCGTTAACTAACGCCTGATTCGCGTGACTTC 3' | + | PCR (605) | 14582 |
| LV195 | 5' ACGTGCGTTAACTAACCGATGGGGAATGGCCAG3' | + | PCR (624) | 14582 |
| LV196 | 5' GGAGTGGTTAACCTCGTCAAGTAACCGATGGGGAATGGCCAG3' | + | PCR (625) | 14582 |
| LV197 | 5' ACGTGCGTTAACGGCCGGTAAAACCAGAGC 3' | + | PCR (626) | 14582 |
| LV198 | 5' GCTCGTGCTAGCCTTTAGCATCACATACAC 3' | + | Nhel —site PCR | 14140 |
| LV200 | 5' ACGTGCTTAATTAACCCAGCAACTGGCACAGTTG 3' | | PCR (635) | 14981 |
| LV201 | 5' ACGIGCITAATITAAATGICATCITCAGCAGCCAG 3' | | PCR (636) | 14981 |
| 1.V202 | 5' ACGTGCTTAATTAACCGCTGGATGAAAGCGACGC3' | | PCR)637) | 14981 |
| LV203 | 5' ACGTGCTTAATTAACGCACTGTATGAGCAACCGG3' | • | PCR (638) | 14981 |
| 1.7204 | 5' ACGTGCTTAATTAACCTTGACTGGCGGATGTAGA 3' | | PCR (639) | 14981 |
| LV216 | 5' ACCAGAGCCAGAAGAAAAAAAAAGTACAGCTCCGATGGGGAG | + | PCR (696) | 14611 |
| | GGTGCAATGAT 3' | | | |
| LV268 | S' ACCAGAGCCAGAAGAAAAAGAAAAGTACAGCTCCGATGGGGA 3' | + | PCR (769) | 14611 |
| LV269 | 5' CTCCGATGGGGAATGGCCAGCCAGTGTTAGAACTGTGCCAGT 3' | + | PCR (769) | 14641 |
| 02011 | ELTOON A COURT A VITTA A A CA A COTTO A CACTOR A TIGGOOF A A COCONTO TO CONTO TO CONTO TO CONTO TO CONTO TO CO | T 12 UL | (970) 120 | |

"The restriction sites are underlined.